

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Claims Listing:**

Claim 1 (previously canceled)

Claims 2-27 (canceled)

Claim 28 (currently amended): A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- (A) receiving the coordinates of a protein backbone structure comprising a plurality of variable residue positions;
- (B) establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
- (C) analyzing the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences, wherein said analyzing step includes a forcefield calculation.

Claim 29 (currently amended): A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- (A) receiving the coordinates of a protein backbone structure comprising a plurality of variable residue positions;
- (B) establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
- (C) analyzing the interaction of either or both of:
  - i) each of said rotamers with all or part of the remainder of said protein backbone structure; and
  - ii) each of said rotamers with all or part of the remainder of the rotamers for each amino acid at each position of said protein; to generate a set of optimized protein sequences, wherein said analyzing step includes a forcefield calculation.

Claim 30 (currently amended): ~~A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:~~  
~~(A) — receiving a protein backbone structure;~~  
~~(B) — establishing a group of potential rotamers for each of said variable residue positions wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and~~  
~~(C) — analyzing the interaction of either or both of:~~  
~~i) — each of said rotamers with all or part of the remainder of said protein backbone structure; and~~  
~~ii) — each of said rotamers with all or part of the remainder of the rotamers for each amino acid at each position of said protein;~~  
~~to generate a set of optimized protein sequences, wherein said analyzing step includes a forcefield calculation; and (D)~~

A method according to Claim 28 or 29, further comprising identifying residues in at least one of said optimized protein sequences that differ from the starting backbone.

Claim 31 (canceled)

Claim 32 (currently amended): A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:

- (A) receiving a protein backbone structure with variable residue positions;
- (B) establishing a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains;
- (C) analyzing the interaction of each of said rotamers with all or part of the ~~remainder~~ remainder of said protein backbone structure to generate a set of optimized protein sequences, wherein said analyzing step includes a Dead-End Elimination (DEE) computation; and
- (D) identifying residues in at least one of said optimized protein sequences that differ from the starting backbone.

Claim 33 (new): A method according to claim 29, further comprising step (D) identifying residues in at least one of said optimized protein sequences that differ from the starting backbone.